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RAW SEQUENCE LISTING   DATE: 02/11/2002
PATENT APPLICATION: US/09/899,429A   TIME: 13:40:42

Input Set : A:\98385Jseq.txt
Output Set: N:\CRF3\02112002\I899429A.raw

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 3  <110> APPLICANT: Hauptmann, Rudolph
 4         Himmler, Adolph
 5         Maurer-Fogy, Ingrid
 6         Stratowa, Christian
 8  <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
 9         Them
11  <130> FILE REFERENCE: 98-385-J
13  <140> CURRENT APPLICATION NUMBER: 09/899,429A
14  <141> CURRENT FILING DATE: 2001-07-03
16  <150> PRIOR APPLICATION NUMBER: 09/792,356
17  <151> PRIOR FILING DATE: 2000-02-23
19  <150> PRIOR APPLICATION NUMBER: 08/477,639
20  <151> PRIOR FILING DATE: 1955-06-07
22  <150> PRIOR APPLICATION NUMBER: 08/383,676
23  <151> PRIOR FILING DATE: 1995-02-01
25  <150> PRIOR APPLICATION NUMBER: 08/153,287
26  <151> PRIOR FILING DATE: 1993-11-17
28  <150> PRIOR APPLICATION NUMBER: 07/821,750
29  <151> PRIOR FILING DATE: 1992-01-02
31  <150> PRIOR APPLICATION NUMBER: 07/511,430
32  <151> PRIOR FILING DATE: 1990-04-20
34  <160> NUMBER OF SEQ ID NOS: 97
36  <170> SOFTWARE: PatentIn Ver. 2.0
38  <210> SEQ ID NO: 1
39  <211> LENGTH: 1368
40  <212> TYPE: DNA
41  <213> ORGANISM: Homo sapiens
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44  <221> NAME/KEY: CDS
45  <222> LOCATION: (1)..(1365)
47  <220> FEATURE:
48  <221> NAME/KEY: sig_peptide
49  <222> LOCATION: (1)..(87)
51  <220> FEATURE:
52  <221> NAME/KEY: misc_feature
53  <222> LOCATION: (88)..(120)
54  <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
55         extracellular proteases following secretion
57  <220> FEATURE:
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59  <222> LOCATION: (606)..(633)
60  <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
61         extracellular proteases following secretion
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66  1               5                  10                  15
68 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct     96
69 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
70              20                  25                  30
72 cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa    144
73 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
74          35                  40                  45
76 tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa    192
77 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
78      50                  55                  60
80 gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac    240
81 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
82 65                  70                  75                  80
84 tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc    288
85 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
86                  85                  90                  95
88 aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg    336
89 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
90              100                 105                 110
92 gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg    384
93 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
94          115                 120                 125
96 aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc    432
97 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
98      130                 135                 140
100 aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag    480
101 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
102 145                 150                 155                 160
104 aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa    528
105 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
106                 165                 170                 175
108 aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg    576
109 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
110                 180                 185                 190
112 aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca    624
113 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
114          195                 200                 205
116 ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt    672
117 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
118 210                 215                 220
120 tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag    720
121 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
122 225                 230                 235                 240
124 tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag    768
125 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
126                 245                 250                 255
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128 ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc   816
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132 ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg   864
133 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
134         275             280             285
136 ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt   912
137 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
138     290             295             300
140 ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg   960
141 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
142 305             310             315             320
144 gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac  1008
145 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
146             325             330             335
148 ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac  1056
149 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
150         340             345             350
152 act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg  1104
153 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
154         355             360             365
156 ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag  1152
157 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
158     370             375             380
160 atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa  1200
161 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
162 385             390             395             400
164 tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc  1248
165 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
166             405             410             415
168 acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc  1296
169 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
170         420             425             430
172 tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg  1344
173 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
174         435             440             445
176 ccc gcg ccc agt ctt ctc aga tga                                  1368
177 Pro Ala Pro Ser Leu Leu Arg
178     450             455
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182 <211> LENGTH: 455
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 2
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191         20              25              30
193 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
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194        35                 40                 45
196 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
197    50                 55                 60
199 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
200 65                 70                 75                 80
202 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
203                85                 90                 95
205 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
206            100                105                110
208 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
209        115                120                125
211 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
212    130                135                140
214 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
215 145                150                155                160
217 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
218            165                170                175
220 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
221            180                185                190
223 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
224        195                200                205
226 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
227    210                215                220
229 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
230 225                230                235                240
232 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
233            245                250                255
235 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
236            260                265                270
238 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
239        275                280                285
241 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
242    290                295                300
244 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
245 305                310                315                320
247 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
248            325                330                335
250 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
251        340                345                350
253 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
254        355                360                365
256 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
257    370                375                380
259 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
260 385                390                395                400
262 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
263            405                410                415
265 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
266            420                425                430
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271 Pro Ala Pro Ser Leu Leu Arg
272     450                 455
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276 <211> LENGTH: 483
277 <212> TYPE: DNA
278 <213> ORGANISM: Homo sapiens
280 <220> FEATURE:
281 <221> NAME/KEY: CDS
282 <222> LOCATION: (1)..(483)
284 <400> SEQUENCE: 3
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286 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
287   1               5                   10                  15
289 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt      96
290 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
291             20                  25                  30
293 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc     144
294 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
295         35                  40                  45
297 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa     192
298 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
299     50                  55                  60
301 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac     240
302 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
303 65                  70                  75                  80
305 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg     288
306 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
307                 85                  90                  95
309 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg     336
310 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
311             100                 105                 110
313 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc     384
314 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
315         115                 120                 125
317 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac     432
318 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
319     130                 135                 140
321 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag     480
322 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
323 145                 150                 155                 160
325 aat                                                                 483
326 Asn
329 <210> SEQ ID NO: 4
330 <211> LENGTH: 161
331 <212> TYPE: PRT
332 <213> ORGANISM: Homo sapiens
334 <400> SEQUENCE: 4
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 02/11/2002
PATENT APPLICATION: US/09/899,429A   TIME: 13:40:43

                    Input Set : A:\98385Jseq.txt
                    Output Set: N:\CRF3\02112002\I899429A.raw

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L:1494 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:2245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:2357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:2432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:2473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:2476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:2495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:2498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:2531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
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